

OPEN READING FRAME: 3543bp

Fig. 1

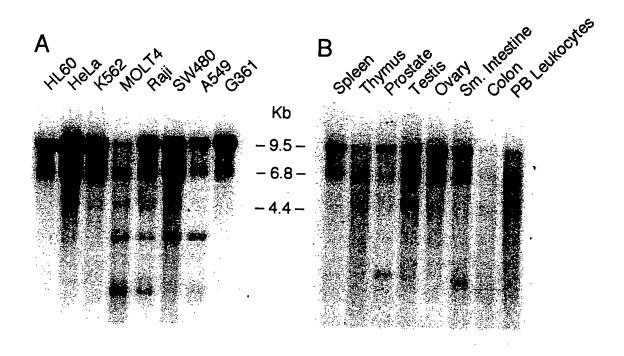


Fig. 2

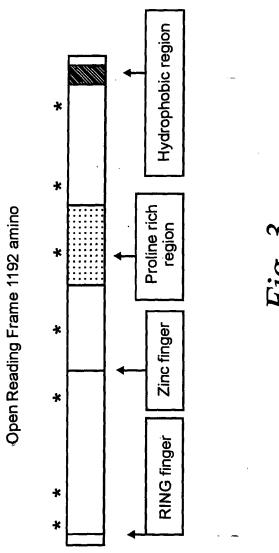


Fig. 3

199

C3HC3D motif

58 80 62 61 182

VKVLECGVCEDV FSL - - QGDKVPRLLLCGHTVCHDCLTRLPLHGR - - AIRCPFDRQVTD KRRLL CPLCGK PMREPVQVST -----CGHRFCDTCLQEFLSEG---VFKCPEDQLPLD - EWRSCFI CTMEY SR TDKNLH-PIIL NCGHNLCRSCINKL---TGNGIVKCPFDR----QEVLCCSI CNRHFNE-----TFLPVSL I CGHVI CRKCAEKPENQTK-----PCPHDDWKTT TEFLS CPIC ---YNEFDENVHKPISLGCSHTVCKTCLNKLHRKA-----CPFDQTAIN DEDLICPICSGVL EEPVQAPH-----CEHAFCNACI TQWFSQQ---Q-TCPVDRSVVT --YSECLVC---Y QKFDENTRIPRVMDCGHTLCDFCINQIVKMAGCYSATCPFDRVRI A. C3HC3D Ring finger homologies C.elegans cDNA EST 3879246 C. elegans cDNA EST 3878739 C. elegans 25.8KD protein H. sapiens SBBI03 H.sapiens CART1 H.sapiens ARD1 **MNAB**

B. C3H Zinc finger homologies

448	136	166	181	235	
ETPQPQPNSKYKTSMCRDLRQQGGCPRGTNCTFAHSQEELEKYRLRNK	HTEYKTRL CDAFRREGYCPYNDNCTYAHGQDELRVPRRRQE	QPMNTSRYKTEL CRPFEEAGECKYGEKCQFAHGSHEL	SSRYKTEL CRPFEENGACKYGDKCQFAHGIHEL	QLPQLVNKTLYKT EL CESFT I KGYCKYGNKCQFAHGLNELK	
	PE-1	ptis 11	TIS11B	CTH1	
MNAB	elegans	nelanogaster	apiens	erevisiae	C3H motif
W	ပ်	D.n	H.s	S.	\mathbb{S}

Fig. 4

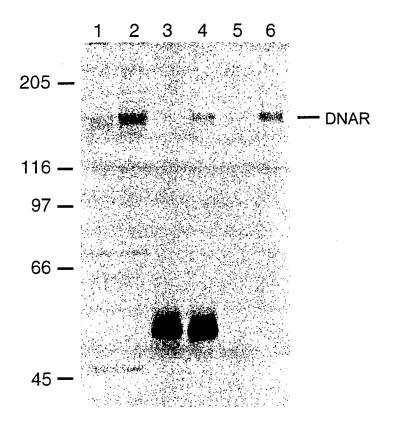


Fig. 5

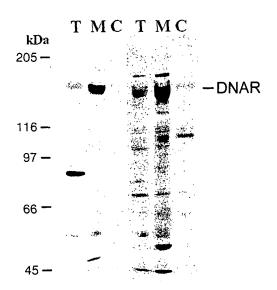
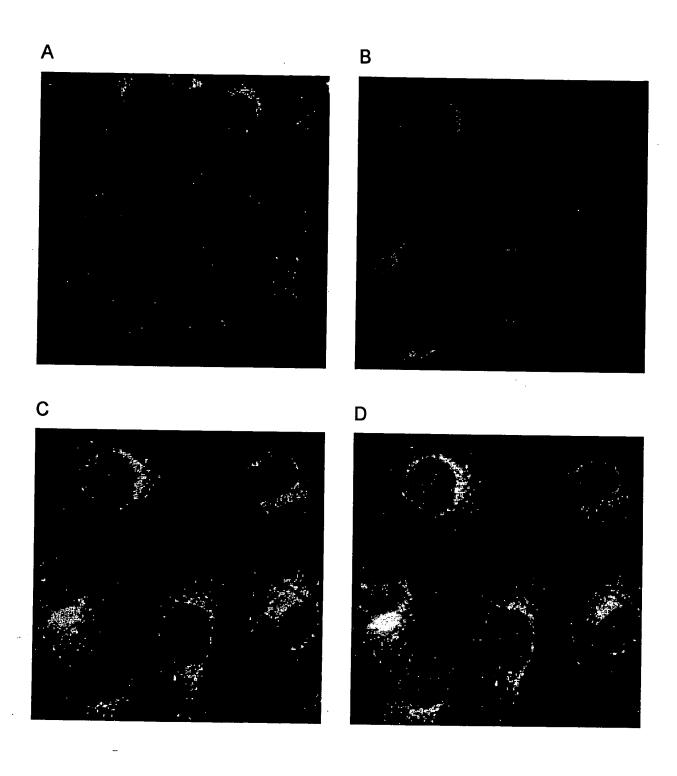
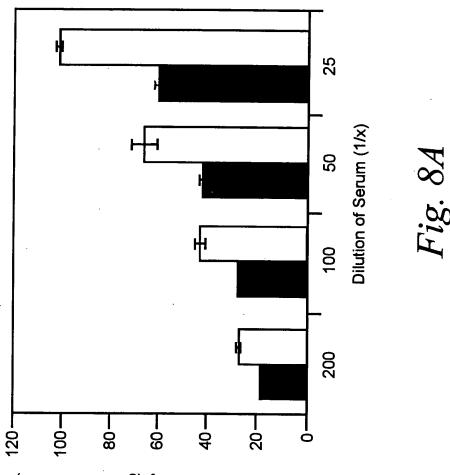


Fig. 6

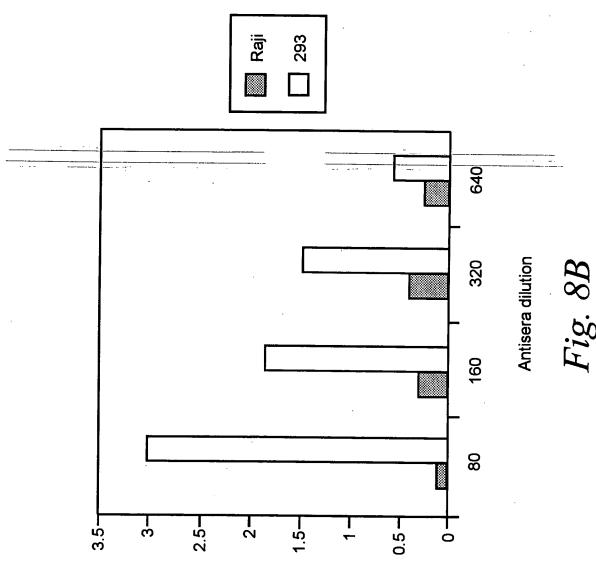


BEST AVAILABLE COPY

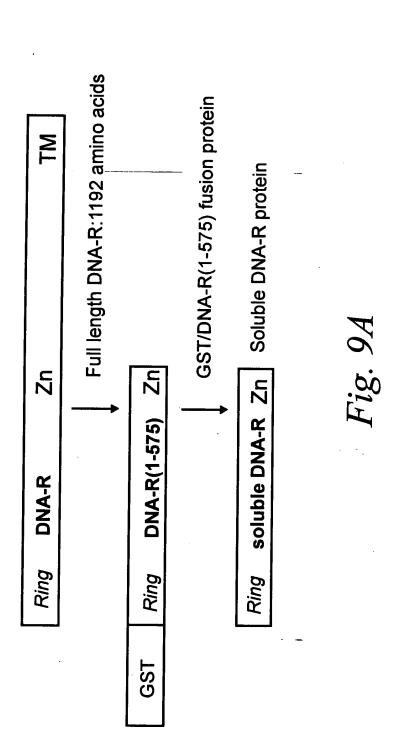
Fig. 7



Fluorescence Intensity (geometric mean)



Fluorescence Intensity



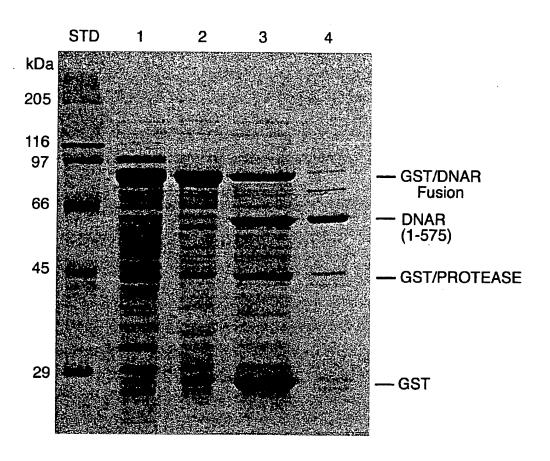


Fig. 9B

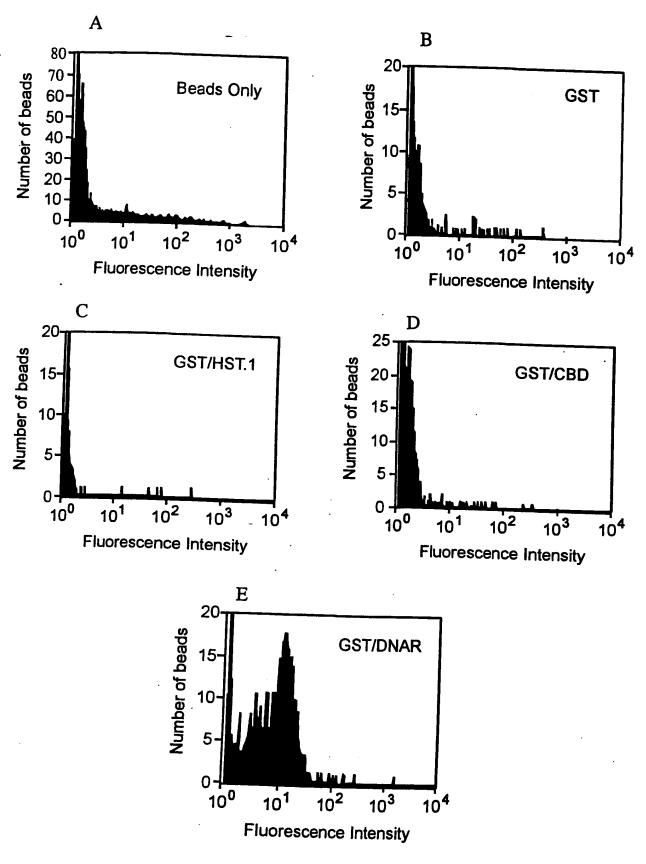


Fig. 10

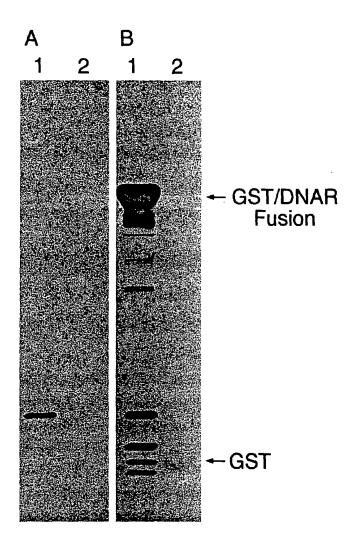
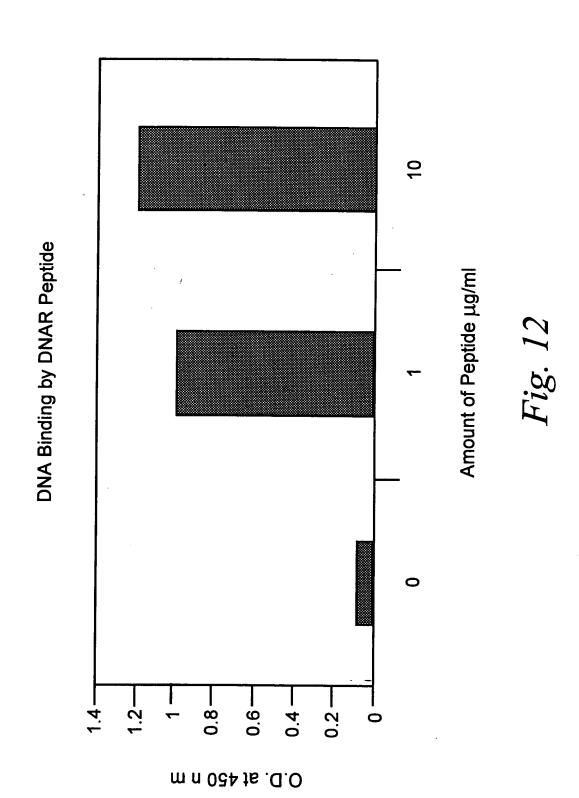
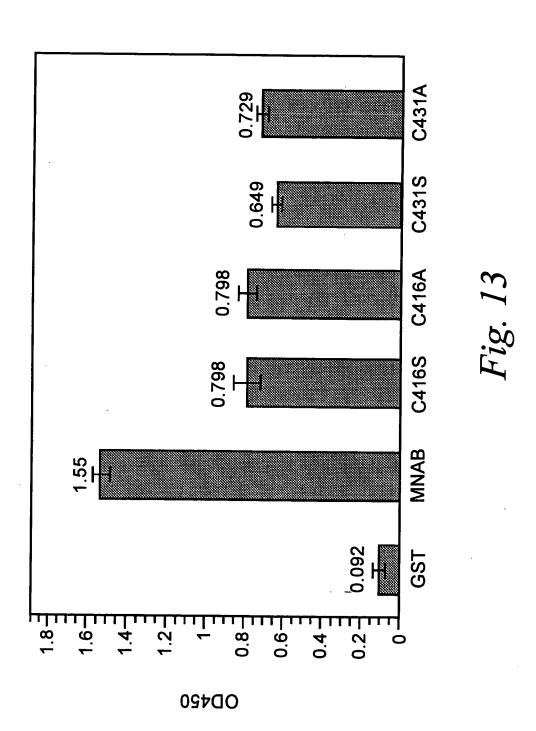
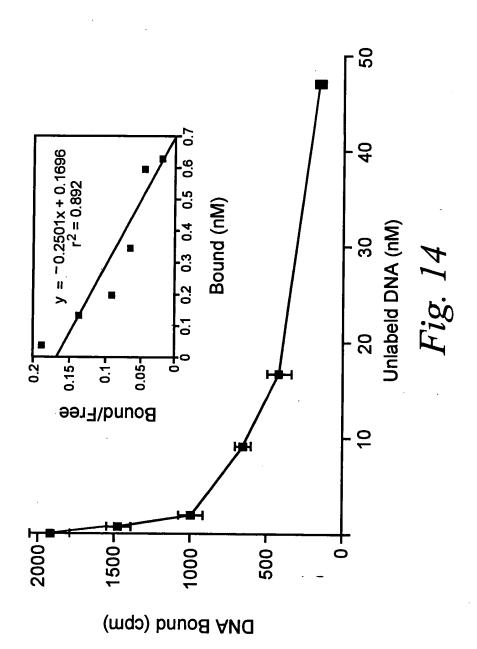
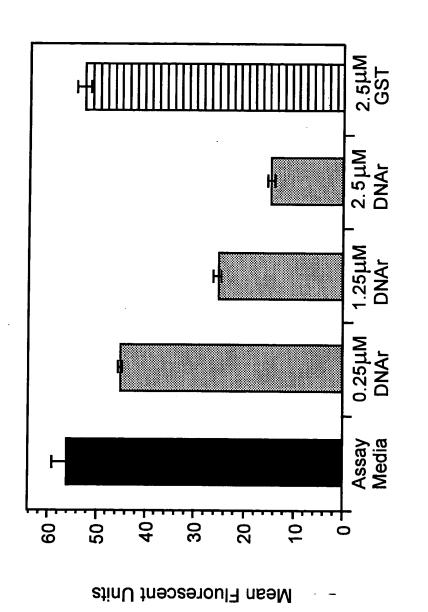


Fig. 11



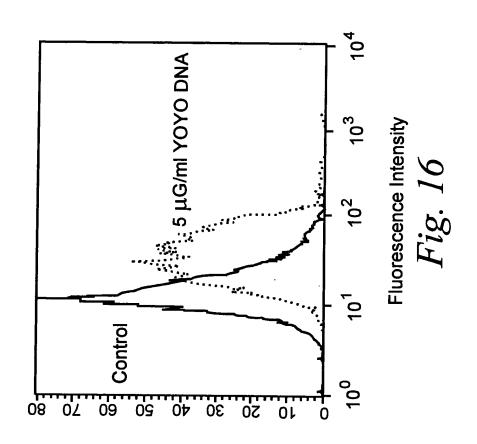




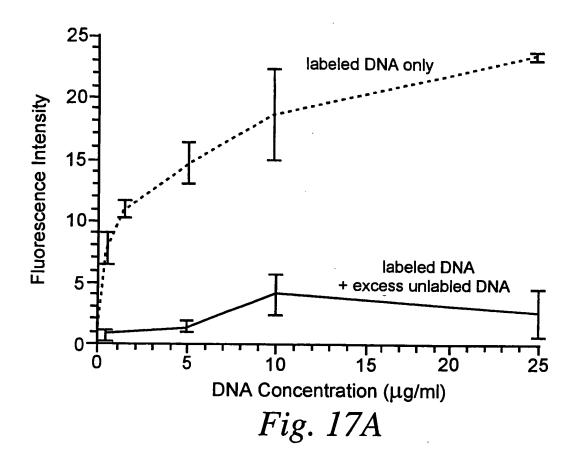


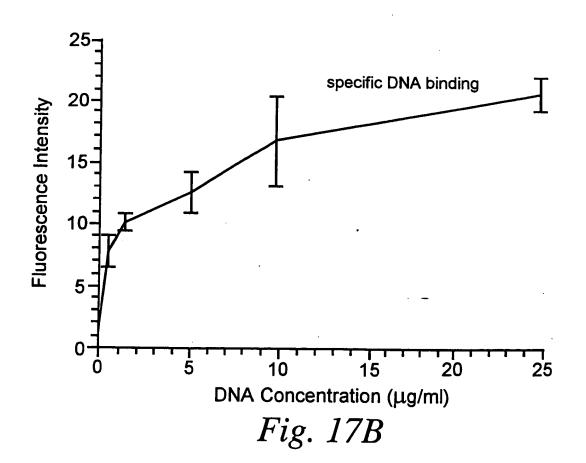
Concentration of Competitor Protein

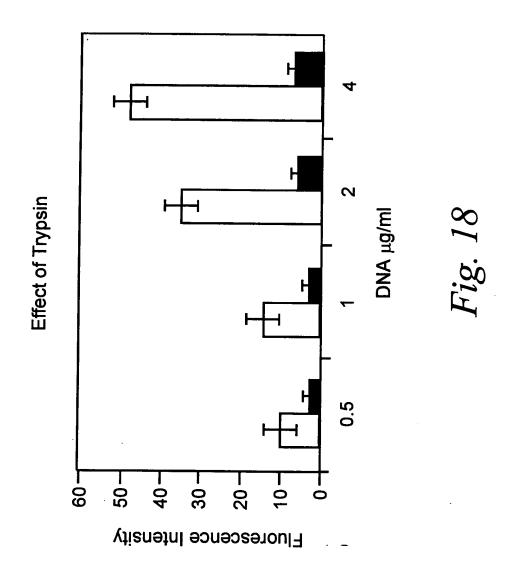
Fig. 15

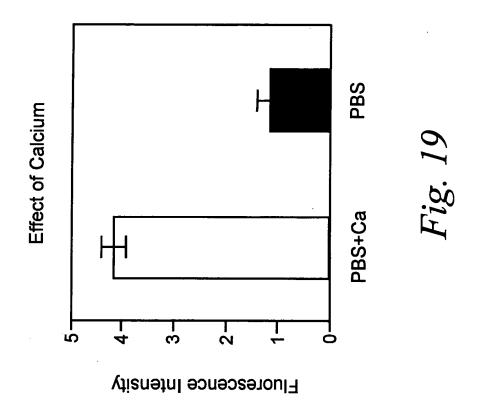


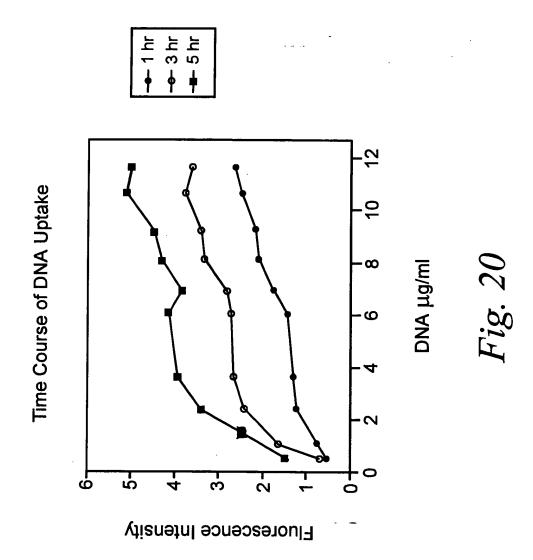
Number of Cells

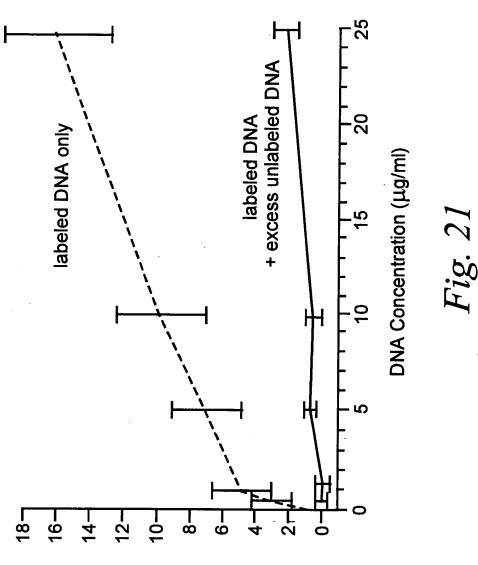




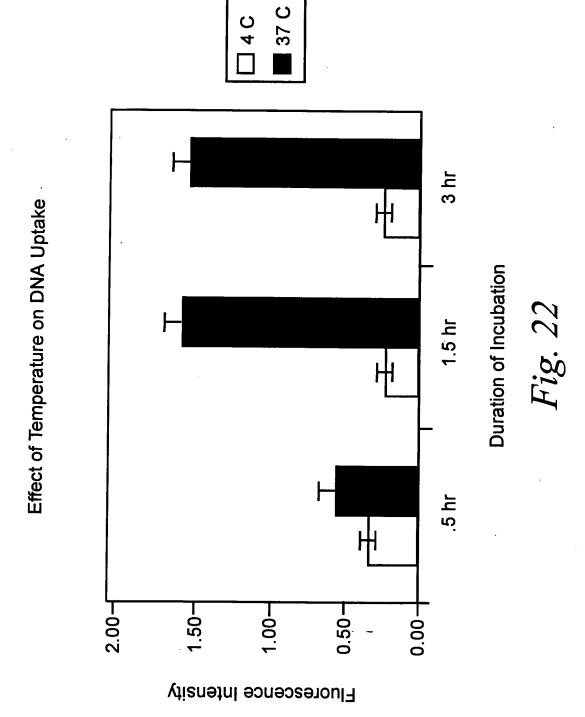




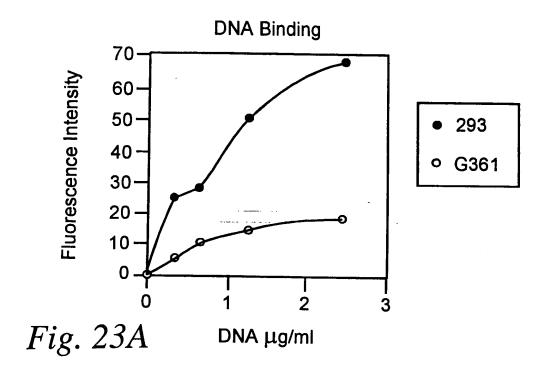




Fluorescence Intensity







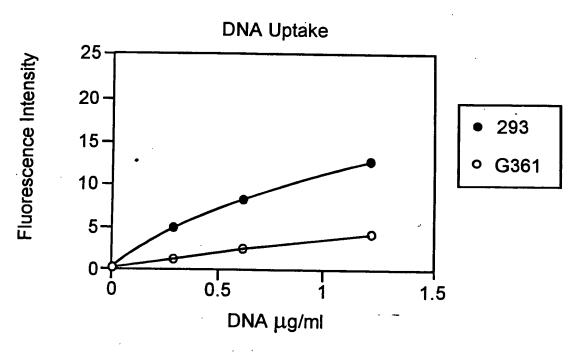


Fig. 23B

